



## RAW SEQUENCE LISTING

DATE: 11/10/2003

PATENT APPLICATION: US/09/424,686F

TIME: 11:29:39

Input Set : A:\pto.ln.txt

Output Set: N:\CRF4\11102003\I424686F.raw

4 <110> APPLICANT: Hagen, Gustav  
 5 Siegmund, Hans-Ulrich  
 6 Weichel, Walter  
 7 Wick, Maresa  
 8 Zubov, Dmitry  
 10 <120> TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and  
 therapeutic  
 11 Use  
 13 <130> FILE REFERENCE: Bayer 10,203  
 15 <140> CURRENT APPLICATION NUMBER: US 09/424,686F  
 17 <141> CURRENT FILING DATE: 1999-11-29  
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP98/03468  
 21 <151> PRIOR FILING DATE: 1998-06-09  
 23 <160> NUMBER OF SEQ ID NOS: 32  
 25 <170> SOFTWARE: Microsoft Word  
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 28 <211> LENGTH: 4042  
 29 <212> TYPE: DNA  
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 37 aggtgctgcc gctggccacg ttcgtgcggc gcctggggcc ccagggtgg cggtggtgc 180  
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85 atgccaagct ctcgtgagcag gagctgacgt ggaagatgag cgtgcgggac tgcgcttggc 1620
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89 tcctggccaa gttctcgcac tggtgatga gtgtgtacgt cgtcgagctg ctgaggtctt 1740
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172 <211> LENGTH: 1132
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2

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177 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
178 1 5 10 15
180 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
181 20 25 30
183 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
184 35 40 45
186 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
187 50 55 60
189 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
190 65 70 75 80
192 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
193 85 90 95
195 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
196 100 105 110
198 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
199 115 120 125
201 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
202 130 135 140
204 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
205 145 150 155 160
207 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
208 165 170 175
210 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
211 180 185 190
213 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
214 195 200 205
216 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
217 210 215 220
219 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
220 225 230 235 240
222 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
223 245 250 255
225 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
226 260 265 270
228 Val Ser Pro Ala Arg Pro Ala Glu Ala Thr Ser Leu Glu Gly Ala
229 275 280 285
231 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
232 290 295 300
234 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
235 305 310 315 320
237 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
238 325 330 335
240 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
241 340 345 350
243 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
244 355 360 365
246 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
247 370 375 380
249 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His

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250      385      390      395      400
252    Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
253              405              410              415
255    Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
256              420              425              430
258    Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
259              435              440              445
261    Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
262              450              455              460
264    Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
265    465              470              475              480
267    Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
268              485              490              495
270    Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
271              500              505              510
273    Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
274              515              520              525
276    Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
277    530              535              540
279    Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
280    545              550              555              560
282    Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
283              565              570              575
285    Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
286              580              585              590
288    Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
289              595              600              605
291    His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
292    610              615              620
294    Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
295    625              630              635              640
297    Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
298              645              650              655
300    Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
301              660              665              670
303    Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
304    675              680              685
306    Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
307    690              695              700
309    Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
310    705              710              715              720
312    Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
313              725              730              735
315    Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
316    740              745              750
318    Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
319    755              760              765
321    Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
322    770              775              780

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324   Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
325   785                               790               795               800
327   Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
328                               805               810               815
330   Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
331                               820               825               830
333   Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
334                               835               840               845
336   Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
337                               850               855               860
339   Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
340   865                               870               875               880
342   Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
343                               885               890               895
345   Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
346                               900               905               910
348   Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
349                               915               920               925
351   Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
352   930                               935               940
354   Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
355   945                               950               955               960
357   Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
358                               965               970               975
360   Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
361                               980               985               990
363   Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
364                               995               1000              1005
366   Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
367   1010                          1015              1020
369   Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
370   1025                          1030              1035              1040
372   Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
373                               1045              1050              1055
375   Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
376                               1060              1065              1070
378   Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
379                               1075              1080              1085
381   Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
382   1090                          1095              1100
384   Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
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387   Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
388                               1125              1130
390 <210> SEQ ID NO: 3
391 <211> LENGTH: 1153
392 <212> TYPE: DNA
393 <213> ORGANISM: Homo sapiens .
395 <400> SEQUENCE: 3

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**VERIFICATION SUMMARY**

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